

FIGURE 1

SEQ ID NO: 1

>STAAU\_R009 nucleotide sequence: 1800  
TTGCGAATAGATCAATCGATCATTAATGAAATAAAAGATAAAACCGACATTTTAGACTTGGTAAGTGAATATGTAAATTAGAAAAGAG  
AGGACGCAATTATATAGGTTTGTGTCCTTTTCATGATGAAAAGACACCTTCATTTACAGTTTCTGAAGATAAACAAATTTGTTCATTGTT  
TTGGTTGTAATAAAAGGTGGCAATGTTTCAATTTACTCAAGAAATTAAGACATATCATTTGTTGAAGCGGTTAAAGAAATTAGGTGAT  
AGAGTTAATGTTGCTGTAGATATTGAGGCAACACAACTCTAACTCAAAATGTTCAATTTCTCTGATGATTTACAAATGATTGAAATGCA  
TGAGTTAATACAAGAAATTTATTATTACGCTTTAACAAGACACAGTCGAAGCGCAACAGCATTAACGTACTTACAAGAACGTTGTTTA  
CAGATGCGCTTATTAAAGAGCGAGGCATTGGCTTTGCCCGATAGCTCACATTTTGTGTCATGATTTTCTTCAAAAAGGGTTACGAT  
ATTGAATTAGCATATGAAGCCGGATTATTATACGTAAACGAAGAAAATTTTCAGTTATTACGATAGATTTTCGAAATCGTATTATGTTTCC  
TTTGAAAAATGCGCAAGGAAGAAATTGTTGGATATTTCAGGTCGAACATATACCGGTCAAGAACCAAAATACTTAAATAGTCTGAAACAC  
CTATCTTTCAAAAAGAAAGTTGTTATACAACTTAGATAAAAGCGGTAAATCAATTAGAAAAATTAGATGAAATCGTATTACTAGAAAGGT  
TTTATGGATGTTATAAAATCTGATACCTGCTGGCTTGAAAAACGTTGTTGCAACAATGGGTACACAGTTGTCAGATGAACATATTACTTT  
TATACGAAAGTTAAACATCAAAATATAACATTAAATGTTTGTATGATGGGATTTTGCAGGTAGTGAAGCAACACTTAAACAGGTCAAAATTTGT  
TACAGCAAGGGCTAAATGTATTTGTTATACAAATTGCCATCAGGCATGGATCCGGATGAATACATTTGTAAGTATGGCAACGATGCATTT  
ACTGCTTTTGTAAAAAATGACAAAAAGTCATTTGCACATTATAAAGTGAGTATATAAAGATGAAATGACATATGACCTTTTCATA  
TGAACGTTATTGAAAGAACTAAGTCATGATATTTCGCTTATGAAATCATCGATTTTGCACAAAGGCTTTAAATGATGTTGCACCAT  
TTTTCAATGTTAGTCCTGAGCAATTAGCTAACGAAATACAATTCAAATCAAGCACCCAGCCAATTATTATCCAGAAAGATGAGTATGGCGGT  
TACATTGAAACCTGAGCCAAATTGGTATGGCACAATTTGACAATTTGAGCCGTCAAGAAAAAGCGGAGCGAGCATTTTAAACACATTTAAT  
GAGAGATAAAGATACATTTTAAATTTATGAAAGTTGATAAGGATAACTTCACAAATCAGCATTTTAAATATGTTATTCGAAGTCT  
TACATGATTTTATGCGGAAATGATCAATATAATATCAGTGATGCTGTGAGTATGTTAATTCAAATGAGTTGAGAGAAACACTAAT  
AGCTTAGAACCAATATAATTTGAATGACGAACCATATGAAAAATGAAATTTGATGATGATGTTCAATGTTTATTAATGAAAAAGGACAAAGAAC  
AATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTAGAATTACAAAAATACTATTACAGCAAAATTTGTTGCTA  
AGAATAAAGAACCGCATGTAG

TCF "SECRET"

SEQ ID NO: 2

>STAU\_R009 amino acid sequence : 599  
LRIDQSIINEIKDKTDILDVSEYVKLEKGRNYYIGLCPFHDEKTPSFTVSEDKQICHCFGCKKGGNVFQFTQEIKDISFVEAVKELGD  
RVNVAVDIEATQSNVQIASDDLQMIEMHELIIQEFYYALTKTVEGEQALTYLQERGFDTALIKERGIGFAPDSSHFCHDFLQKKGYD  
IELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIFQKRKLLYNLDKARKSIRKLDEIVLLEG  
FMDVIKSDTAGLKNVVATMGTOQLSDEHITFIRKLTSNITLMFDGDFAGSEATLKTGQNLQQLNVFVIQLPSGMDPDEYIGKYGNDAF  
TAFVKNDDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVSPQLANEIQFNQAPANYYPEDEYGG  
YIEPEPIGMAQFDNLSRQEKAEAFKHLMRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI  
SLEQYNLNDEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAKNKERM

## FIGURE 2

SEQ ID NO: 3

>96ORF078 nucleotide sequence  
ATGAATATAATGCAATTCAAAAGCTTATTGAAATCGATGTATGAAGAGACAAAGCAAAGC  
GACCCGATTGTAGCAAATGTATATCGAGACTGGTTGGCGGTCAATAGATTGTTGGAC  
AATAACGAGTTATCGCCCTTTCGATGATTACGACAGAGTTGAAAAGAAAATCATGAATGAA  
ATCAACTGGAAGAAACACACATTAAGGAGTGTAA

SEQ ID NO: 4

>96ORF078 amino acid sequence 96\_NT|10148-10363|  
MNIMQFKSLLKSMYEETKQSDPIVANVYIETGWAVNRLLDNNELSPFDDYDRVEKKIMNE  
INWKKTHKEC

FIGURE 3

A.

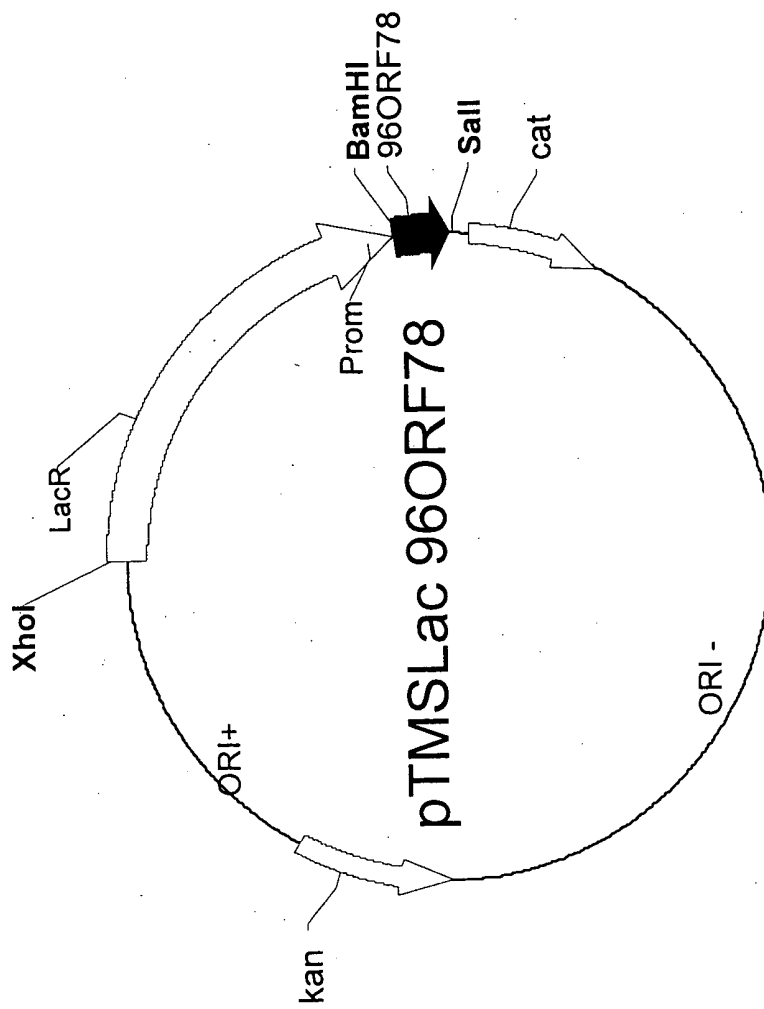


FIGURE 3 B.

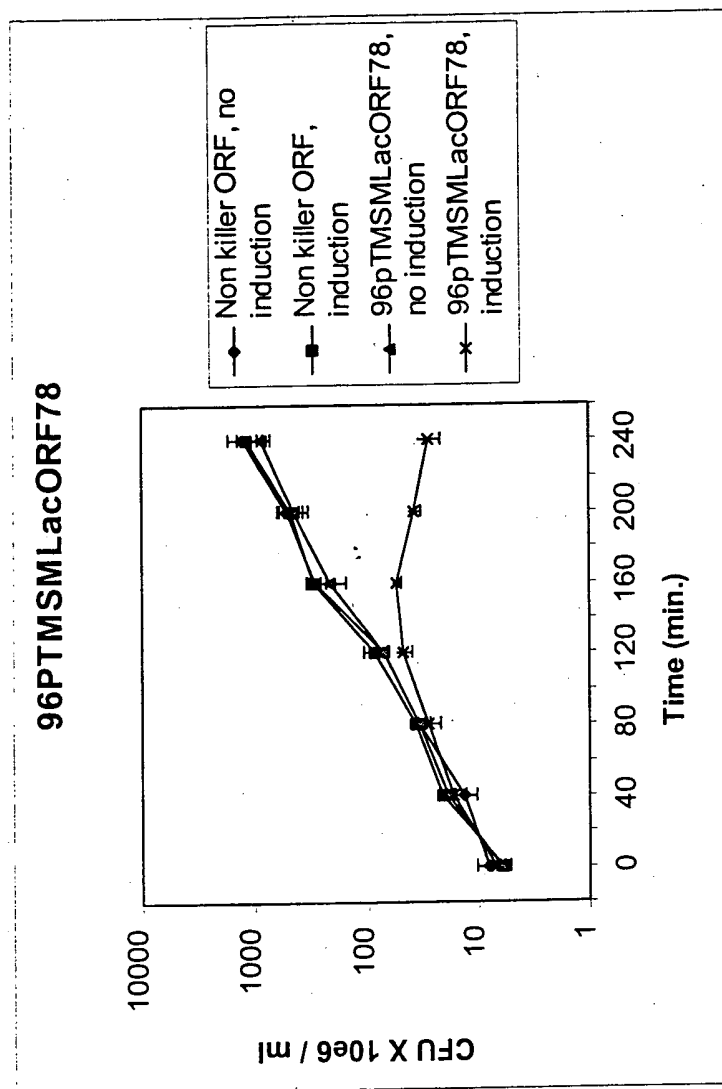
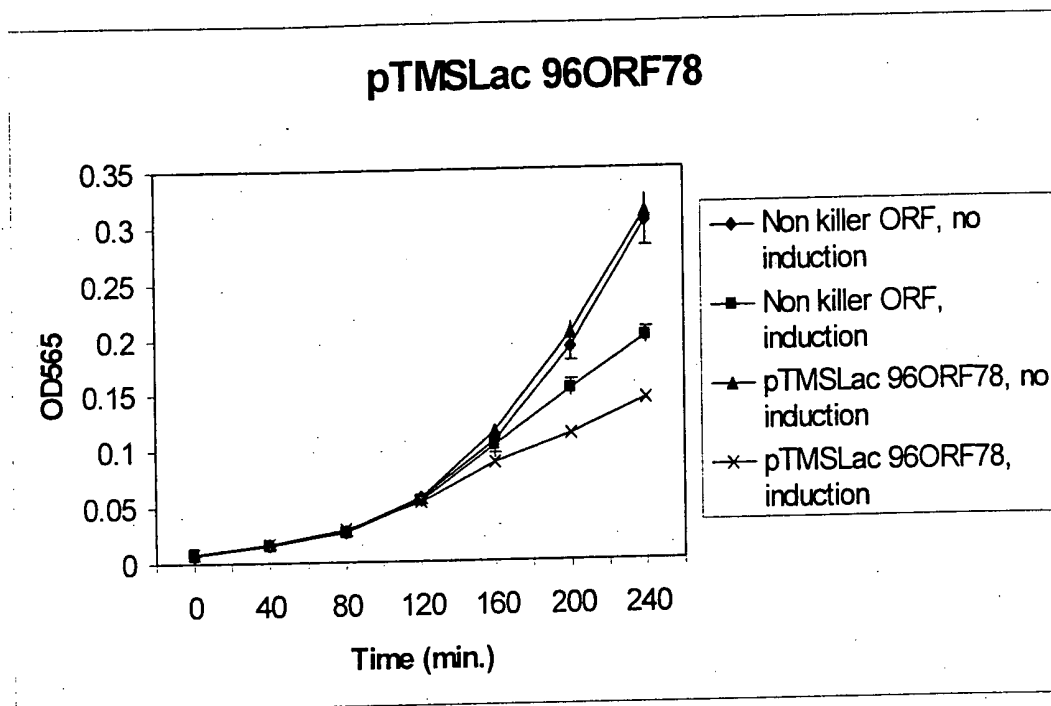


FIGURE 3 C.



D.

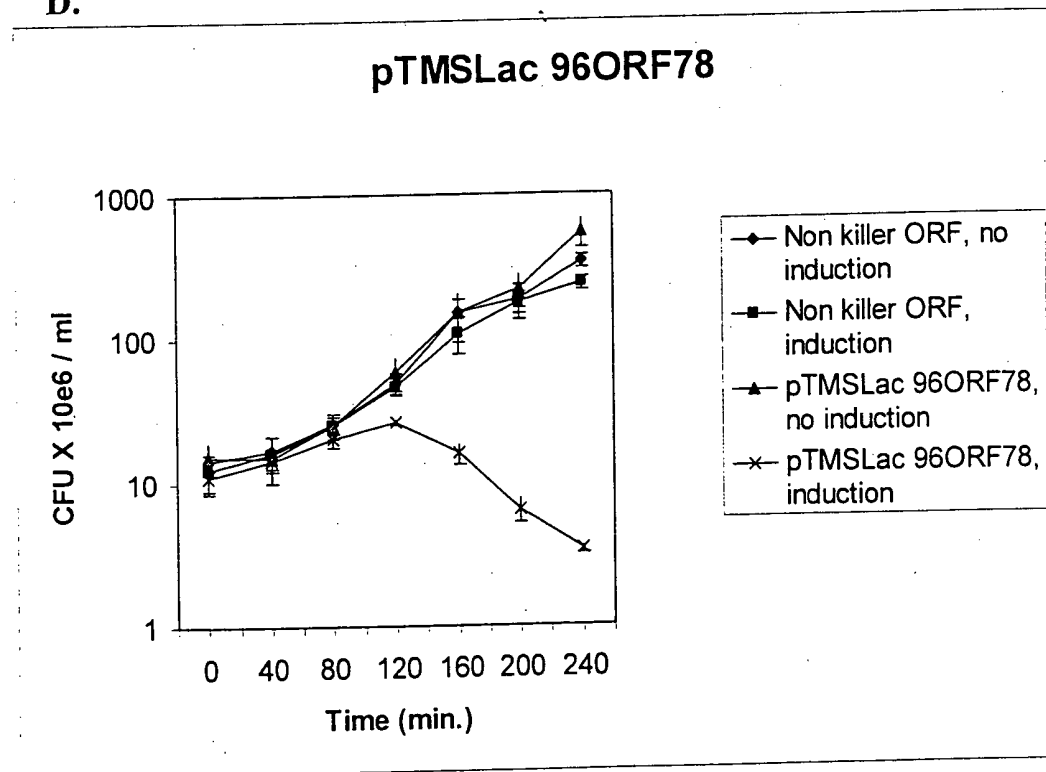
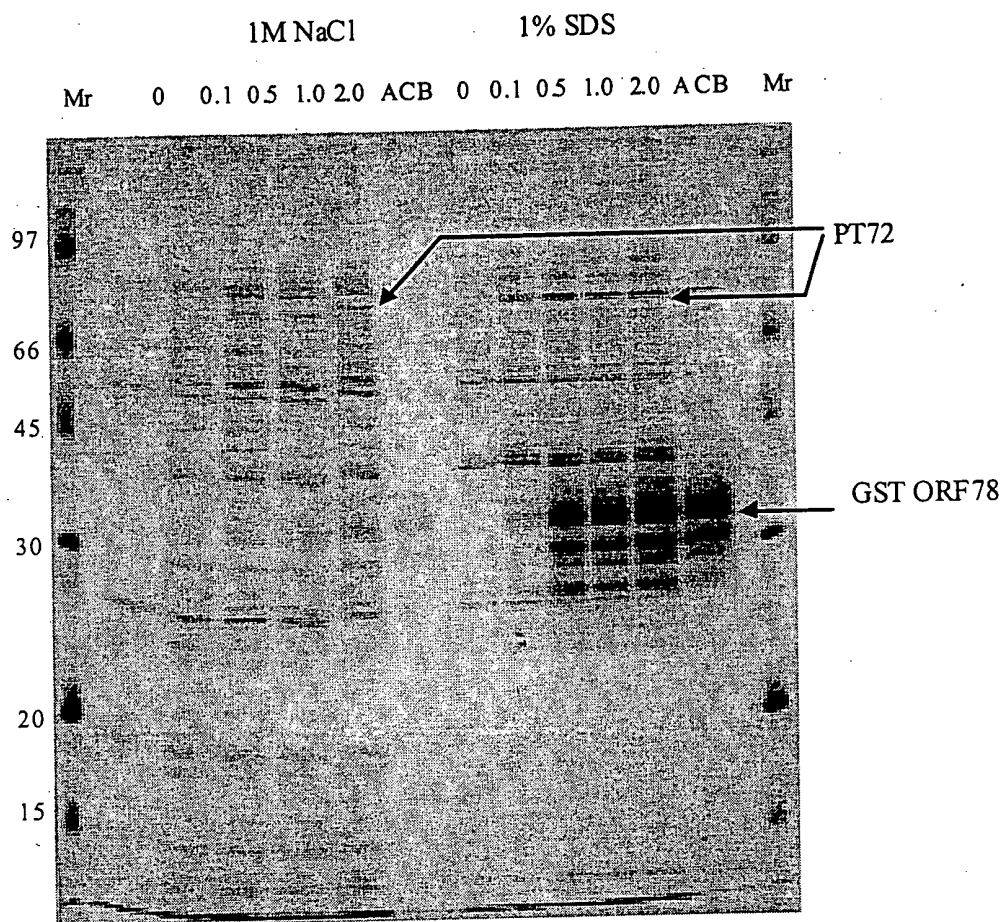


FIGURE 4

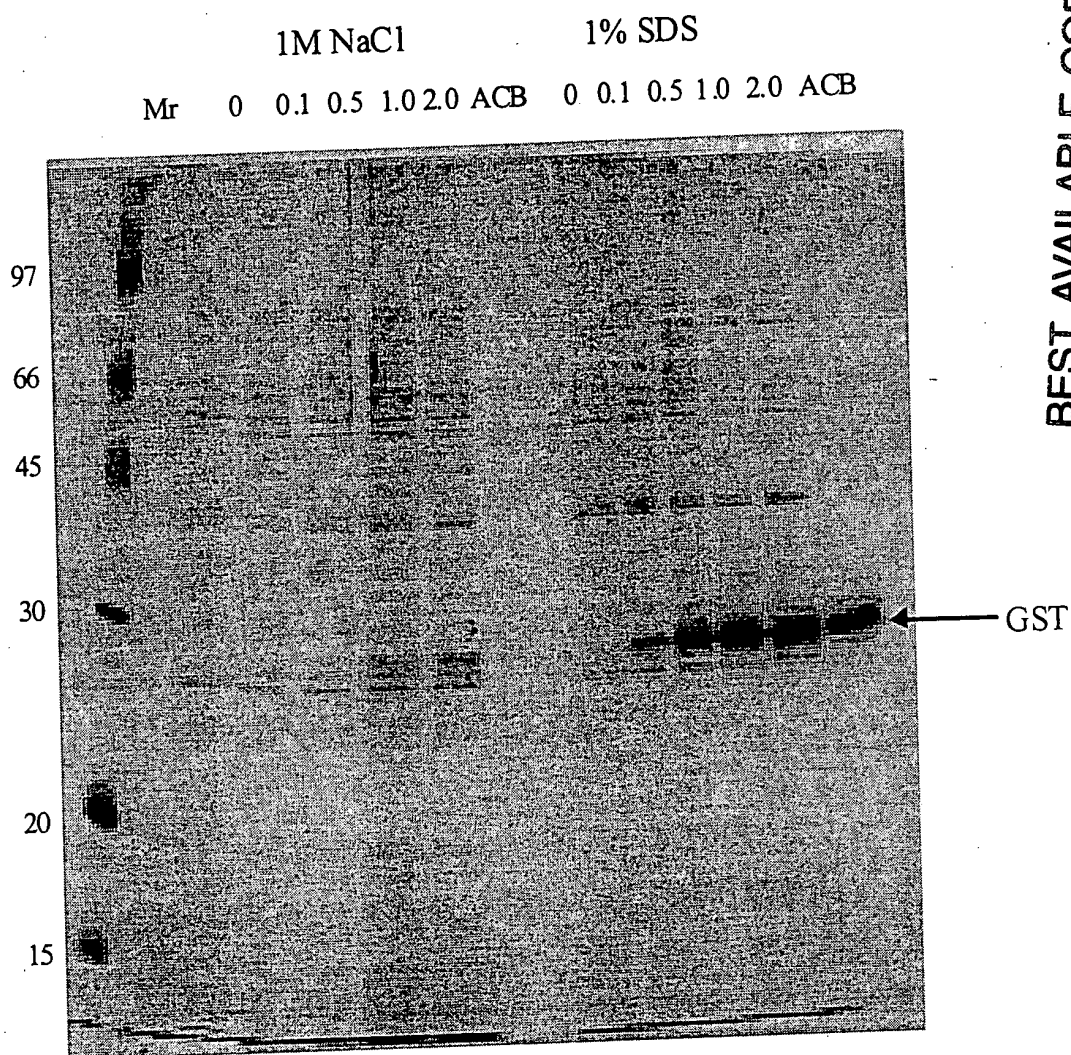
A. GST/96ORF78



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FIGURE 4

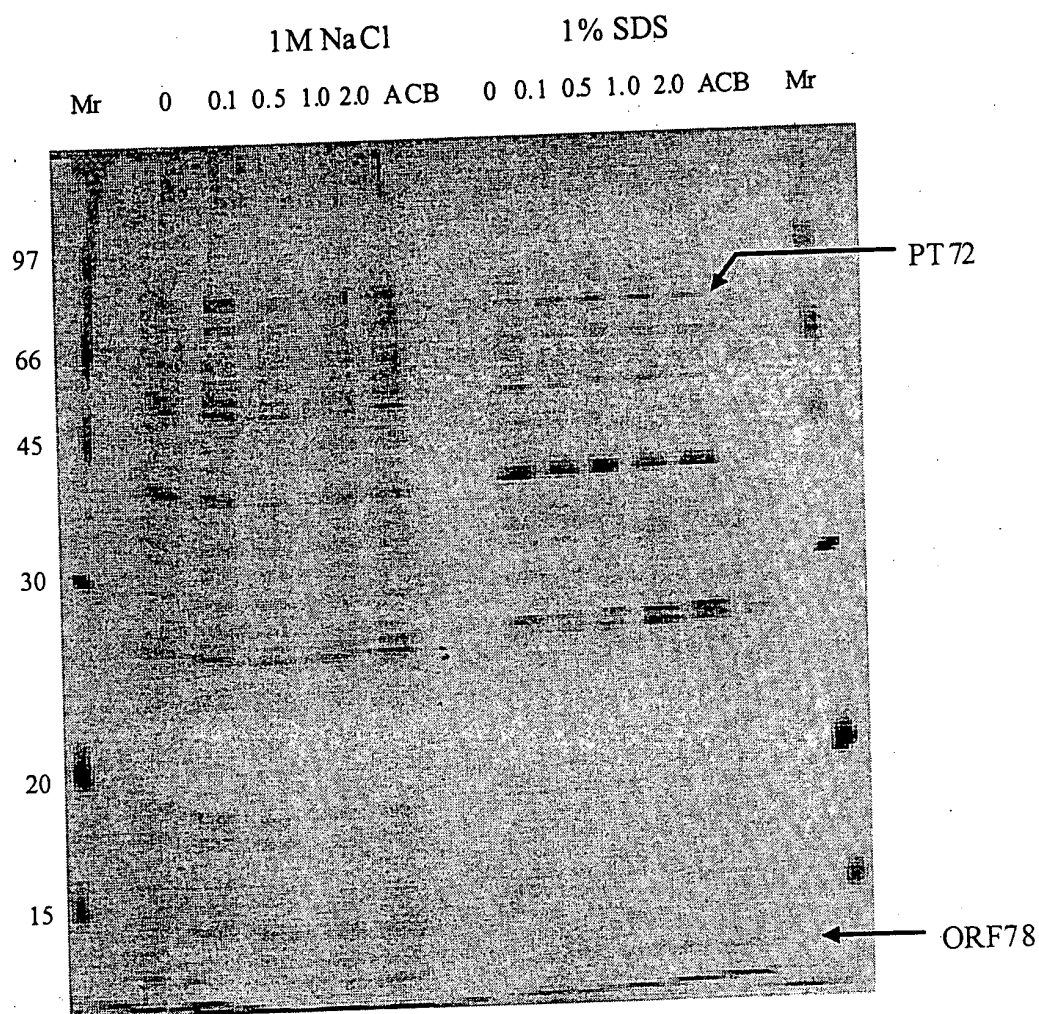
B. GST



BEST AVAILABLE COPY



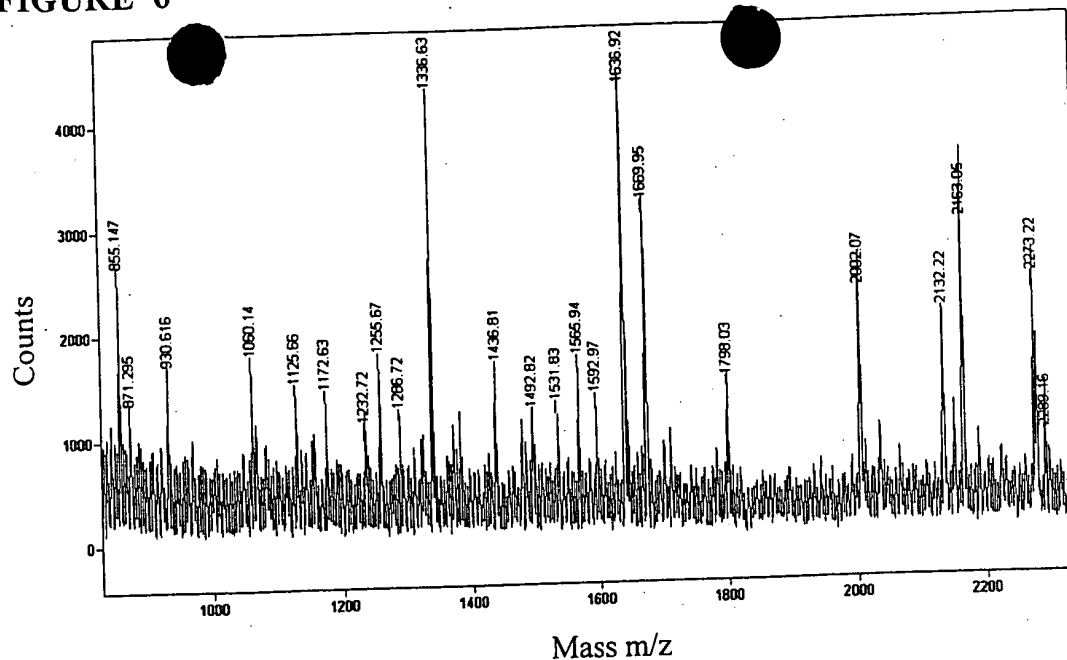
**FIGURE 5 96ORF78 (GST removed)**



10035322 13491

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FIGURE 6



TOGETHER "2252001"

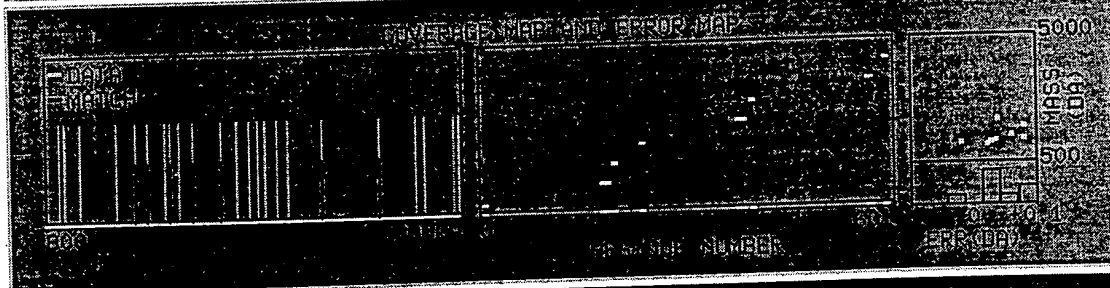
ouContig286: 82020 to 83822: Frame 3 601 aa

Sample ID : orf78 72 [Pass:0]

Measured peptides : 23

Matched peptides : 7

Min. sequence coverage: 14%



1124.649	M	1124.622	0.027	588	596	0	YYLQQIVAK
1171.623	M	1171.590	0.033	394	403	0	ELSHDISLMK
1171.623	M	1171.644	0.021	5	14	0	IDOSINEIK
1254.661	M	1254.620	0.041	563	573	0	GOETIESLNHK
1335.627	M	1335.536	0.091	193	202	0	NEENESYYDR
1435.802	M	1435.734	0.068	233	244	0	YLNSPETPIFOK
1797.019	M	1796.930	0.089	177	192	1	KGYDIELAYEAGLLSR
2001.060	M	2001.016	0.044	374	390	1	VSILKDEIAHNDLSYER

855.147 871.295 930.616 1060.140 1232.717 1286.716 1492.822 1531.830 1565.943 1592.967  
1636.921 1669.948 2132.217 2163.048 2273.222 2289.164

FIGURE 7A

A. Pfam HMM search results

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value
zf-CHC2	3	100	1	98	198.4	1.1e-55
Toprim	260	339	1	151	71.9	1.3e-17

Alignments of top-scoring domains:

zf-CHC2:  
domain 1 of 1, from 3 to 100: score 198.4, E = 1.1e-55  
\*->ipeesIdeLknriDIVdvisYvKkGrnYkgLCPFHdEKTSPFs  
i++++I+e+k+++DI d++seYvKL+K+GrnY+gLCPFHdEKTSPF+  
gi|133988 3 IDQSIINEIKDKTDILDVSEYVVKLEKGRNYIGLCPFHDEKTPSFT 49

gi|133988 50 VSEDKQICHCFGCKKGGNVFQFTQEIKDIDISFVEAVKELGDRVNVAVDIEA 99  
Vs +Kq+ hCFGc++gG+++ F +++++sFvEAv++L dr+++ +++  
VspeKqfYhCFGCGagGdaIkFlmkyeklsFvEAvekLAdragidlpyek  
g<-\*  
+  
gi|133988 100 T 100

# Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17

```

*->kvliiVEgpsdakalagkpskrkivyelpggkdgnvvaslGhlv
+++++ Eg++d+++ a+ +nvva++G+
gi|133988 260 DEIVLLEGFMDVIKSDTAGL-----KNVVATMGQTQ- 289

dLptpegyddkykwlwlpivdvkkgfepyyqiefdqlckcskkidlkkeql
+++++ LSDEHI 295

kllkklakkadevilatDpDreGeaiawkllellkpygpveleddkkvrr
+++++ +l++D+D +G ++++k +l+ +g +v++
gi|133988 296 TFIRKLTSN---ITLMFDGDGFAGSEATLKTGQNLLQQGL-----NVFV 335

iflp<-*
i+lp
gi|133988 336 IQLP 339

```

FIGURE 7B

B. Optimal global alignment of amino acid sequences

Sequence 1 sp|O05338|PRIM\_STAAU DNA PRIMASE (EC 2.7.7.-) - S. aureus. (572 letters)

Sequence 2 STAAU\_R009 STAAU\_R009\_NT|1-1800| (599 letters)

Identical: 560/605 (92%), Similar: 564/605 (93%), Gap: 39/605 (6%)

seq1	1	M-----	27
seq2	1	LRIDQSIINEIKDKTDILDVSEYVVKLEKRGRNYIGLCPFHDEKTPSFTVSEDKQICHCF	60
seq1	28	GCKKGGNVFQFTQEIKDISFVEAVKELGDRNVAVDIEATQSNSNVQIASDDLQMIEMHE	87
seq2	61	GCKKGGNVFQFTQEIKDISFVEAVKELGDRNVAVDIEATQSNSNVQIASDDLQMIEMHE	120
seq1	88	LIQEFYYALTKTVEGEQALTYLQERGTDALIKERGIGFAPDSSHCHDFLQKKGYDIE	147
seq2	121	LIQEFYYALTKTVEGEQALTYLQERGTDALIKERGIGFAPDSSHCHDFLQKKGYDIE	180
seq1	148	LAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIF	207
seq2	181	LAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIF	240
seq1	208	QKRKLLYNLDKARKSIRKLDLDEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEHITFIRK	267
seq2	241	QKRKLLYNLDKARKSIRKLDLDEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEHITFIRK	300
seq1	268	LTSNITLMFDGDFAGSEATLKTGQHLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTTFV	327
seq2	301	LTSNITLMFDGDFAGSEATLKTGQNLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTAFV	360

# "06Feb" 22300T

seq1	328	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQOKAINDVAPFFNVS	387
seq2	361	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQOKALNDVAPFFNVS	420
seq1	388	PEQLANEIQFNQAPANYYPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRREKAERAFKLHL	447
seq2	421	PEQLANEIQFNQAPANYYPE-----DEYGGYIEPEPIGMAQFDNLSRQEKAEARAFKLHL	474
seq1	448	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI	507
seq2	475	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI	534
seq1	508	SLEQYNLNGEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQOIIVAK	567
seq2	535	SLEQYNLNDEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQOIIVAK	594
seq1	568	NKERM	572
seq2	595	NKERM	599

**Sequence 1** STAAU\_R009 (599 letters)  
**Sequence 2** gi|9910841|sp|Q9X4D0|PRIM\_BACST DNA PRIMASE(597 letters)

**Identical:** 209/609 (34%), **Similar:** 315/609 (51%), **Gap:** 22/609 (3%)

seq1	1	L--RIDQSIINEIKDKTDILDVSEYVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICH	58
		:    :     :   : : :                  :  :	
seq2	1	MGHRIPREETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFSVSPEKQIFH	60
seq1	59	CFGCKKGGNVFQFTQEIKDISFVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQ-MIE	117
		: :            :   :  :   :	
seq2	61	CFGCGAGGNAFTFLMDIEGIPFVEAAKRLAAKAGVDLSVYELDVGRDDGGQTDEAKAMTE	120
seq1	118	MHELIQEFYYALTKTVEGEQALTYLQERGFDTALIKERGIGFAPDSSSHFCHDFLQKKGY	177
		::   ::       :             :      :    :	
seq2	121	AHALLKRFYHLLVHTKEGQAALDYLAQRGWTKETIDRFEIGYAPDAPDAAAKLLESHSF	180
seq1	178	DIELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRYYTGQEPKYLNSPET	237
		: : :     :  :            : : :     :      :	
seq2	181	SLPVMKAGLLTKKEDG-RYVGRFRNRIMFPIDHRGETVGFSGRLLGEGHPKYVNSPET	239
seq1	238	PIFOKRKLLYNLDKARKSIRKLDEIVLLEGFMDVIKSDTAGLKNVVATMGTLQSDHEHITF	297
		: :    :  :          :          :   : :        ::	
seq2	240	PVFRKGAILYHFHAARVPIRKRQEALLVEGFADVISAAQAGIDYAIATMGTSLTEEQARI	299
seq1	298	IRKLTSNITLMFDGDFAGSEATLKTGQNLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFT	357
		:     : :           :         :           :	
seq2	300	LRP-CDTITICYDGDGRAGIEAAWAAAEQLSALGCRVKVASLPNGLDPDEYIRVYGGGERF-	357
seq1	358	AFVKNDKKSFAYHKVSILKDEIAHNDLSYE----RYLKELSHDISLMKSSILQQKALNDV	413
		: : :   :    :   :  :    :     :   :   :	
seq2	358	AGEAGCRRPLVAFKMAYLR---RGKNLQHEGERLRYIDEALREIGKLSSPVEQDYLLRQL	414

# FASTA format

```

seq1 414 APFFNVSPEQLANEIQFNQAPANYYPEDGYIEPEPIGMAQFDNLSRQEKAEAF LKH 473
      | | : | | : : | | | | | | | | : | | | | |
seq2 415 AEEFSLSLHEQLSRQRETKPREAPDGETARP---MLAKKLLPAFQNAERLLLAH 470

seq1 474 LMRDKDTFLNYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELRETL 533
      : | | : | | | : : : | | | : : : | | :
seq2 471 MMRSRDVALVVQERIG-GRFNIEEHRALAAYYAFYEEGHEADPGALISRI-PGELQPLA 528

seq1 534 ISLEQYNLNDEPYENEIDDYV-NVINEKGQETIESLNHKLREATRIGDVELQYYLQQIV 592
      : : | : | : | : | : : : | | | | : : :
seq2 529 SDVSLLLIADDVSEQELEDYIRHVLNRPKWLMLKVKEQEKTEAERRKDFLTAARIAKEMI 588

seq1 593 AKNK--ERM 599
      |
seq2 589 EMKKMLSSS 597

```





# FOET "22222222"

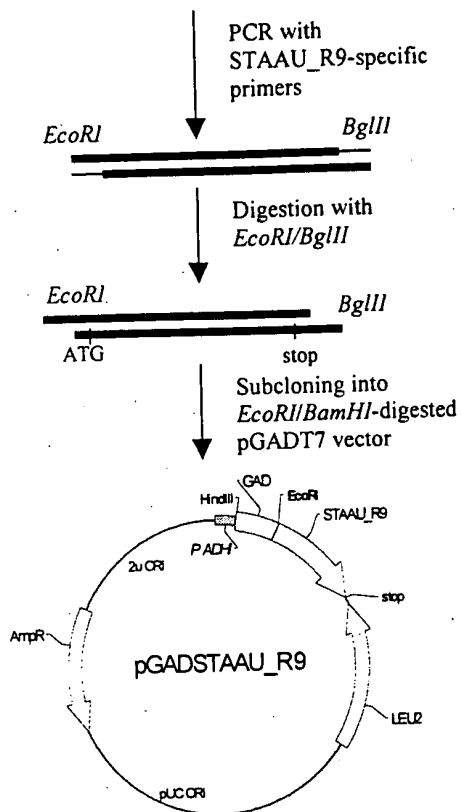
seq1	359	FVKNKKSF	AHKVSIL-KDEIAHNDLSYERYLKELSHDISLMKSSILQOKALNDVAPFF	417
seq2	361	DIIDASVTVM	AFKMQYFRKGNLSDEGDRLAYIKDVLKEISTLSGSLEQEVYVKQLASEF	420
seq1	418	NVSPEQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQ-----EKAERAF		470
seq2	421	SLSQESL	TE--QLSVFSKQNKPADNSG----ETKTRRAHLTTKARQKRLRPAYENAERLL	474
seq1	471	LKHLMRDKDTFLNYYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELR		530
seq2	475	LAHMLRDRSVIKKVIDRVGFQFNIDEH-RALAAAYLYAFYEEGAELTPQHLMARVTDDHIS		533
seq1	531	ETLISLEQYNLNDEPYENEIDDYV-NVINEKQGETIESLNHKLREATRIGDVELQKYYLQ		589
seq2	534	QLLSDILMLQVNQELSEAELSDYVKKVLNQNRNWSMIKEKEAERAEARQKDFLRAASLAQ		593
seq1	590	QIVAKNKERM	599	
seq2	594	EIVTLNRSLK	603	

[illegible]



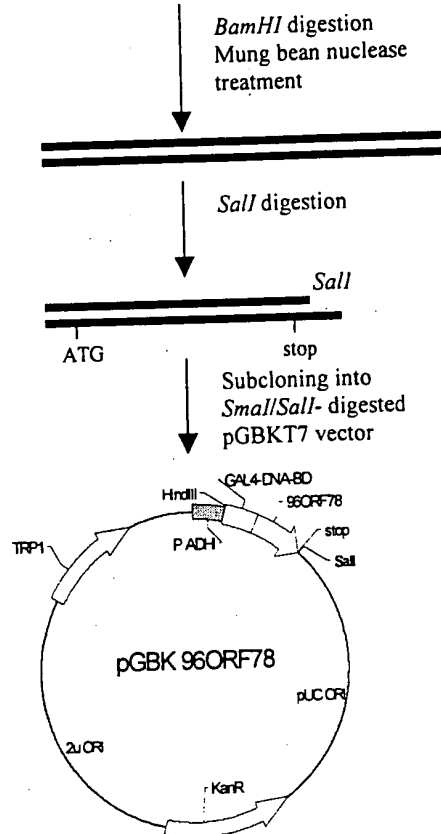
FIGURE 8

A- *Staphylococcus aureus* genomic DNA



B-

96pTMSMLacORF78



C-

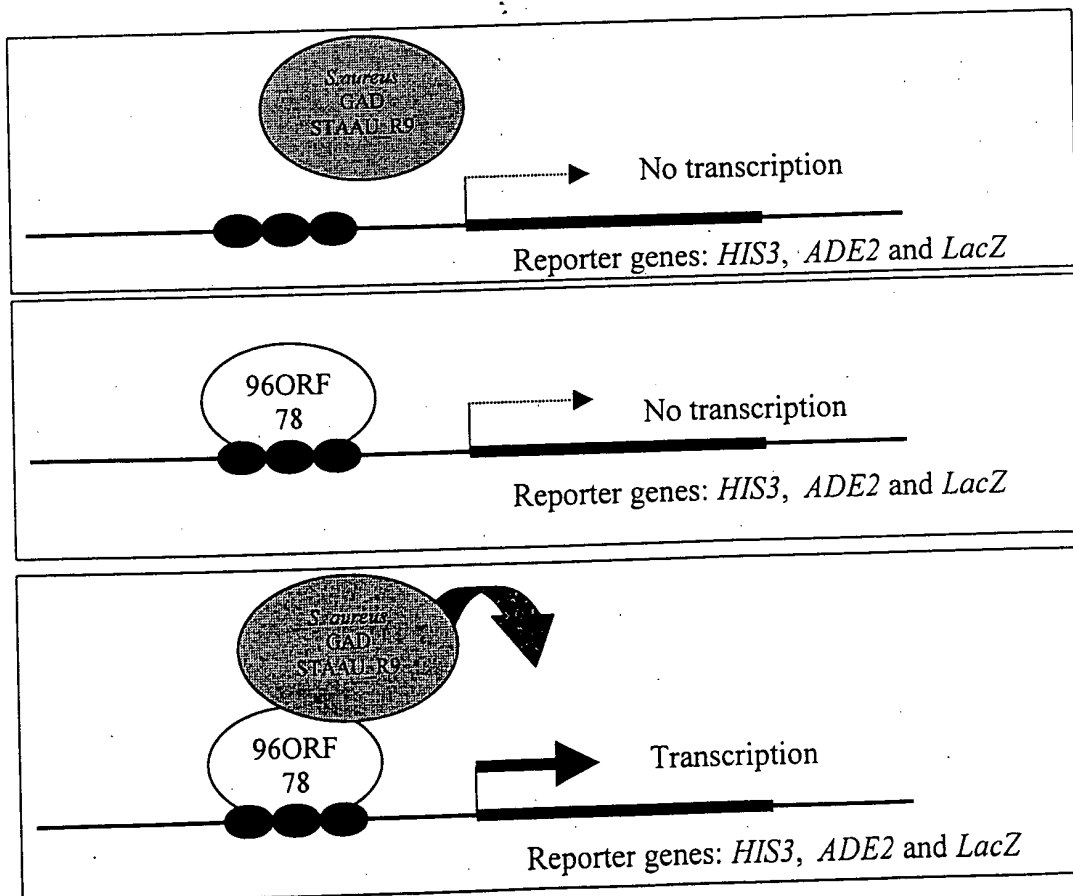
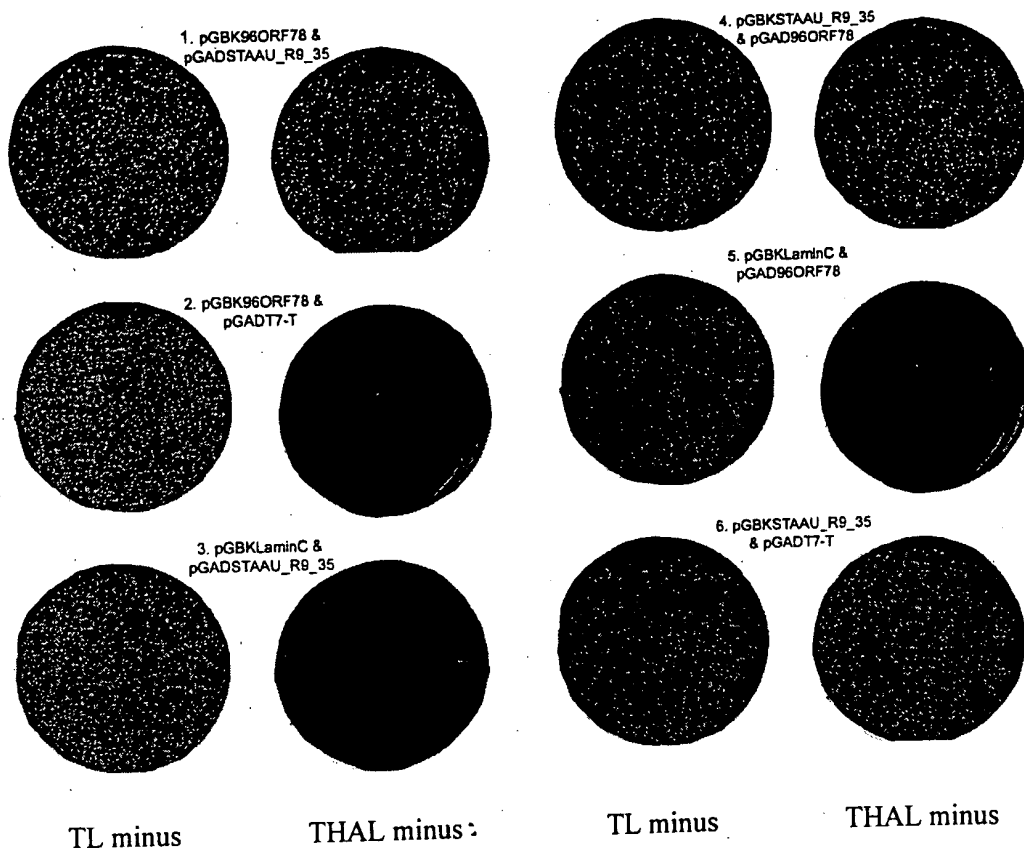
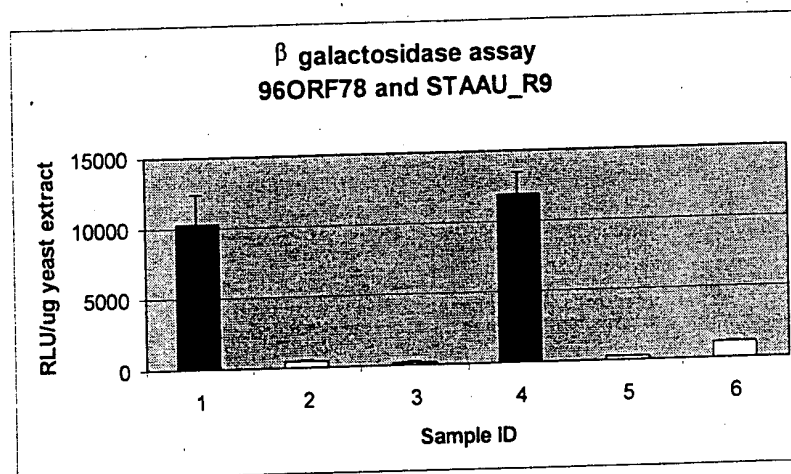


FIGURE 9

A.



B.



Sample	Yeast co-transformants		RLU (avg)	SD
	Plasmid 1	Plasmid 2		
1	pGBK 96ORF78	pGADSTAAU_R9_35	10,250	2,080
2	pGBK 96ORF78	pGADT7-T	475	38
3	pGBK Lamin C	pGADSTAAU_R9_35	224	10
4	pGBKSTAAU_R9_35	pGAD 96ORF78	11,935	1,477
5	pGBK Lamin C	pGAD 96ORF78	243	12
6	pGBKSTAAU_R9_35	pGADT7-T	1,121	37

FIGURE 10

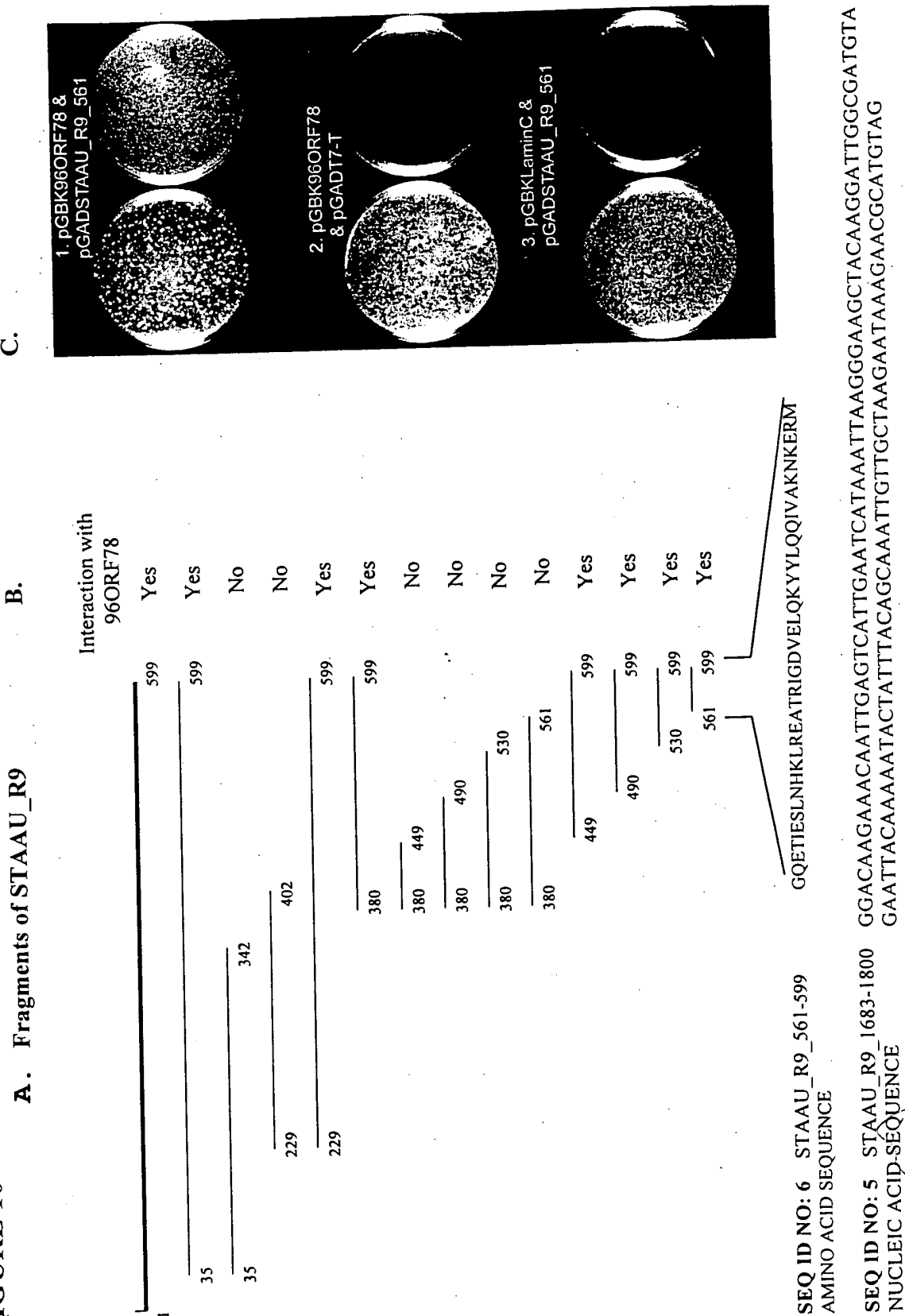


FIGURE 11

A.

	Primer name	Primer sequence 5' → 3'	Restriction site
SEQ ID NO: 8	R9_5E3	5'-ccggaattcTTGCGAATAGATCAATCG-3'	EcoRI
SEQ ID NO: 9	R9_3BG	5'-ggaagatctCTACATGCGTTCTTTATTTC-3'	BglII
SEQ ID NO: 10	R9_5E	5'-ccggaattcATGATAGGTTTGTCCT-3'	EcoRI
SEQ ID NO: 11	R9_5E1	5'-ccggaattcCCAAAATACCTAATAGTCC-3'	EcoRI
SEQ ID NO: 12	R9_5E2	5'-ccggaattcGCACATAATGACCTTTCA-3'	EcoRI
SEQ ID NO: 13	R9_342R	5'-cgcggaattcATGCTGATGGCAATTG-3'	BamHI
SEQ ID NO: 14	R9_402R	5'-ccatcgatGATTTTCATAAGCGAAATATC-3'	Clal
SEQ ID NO: 15	R9_449F	5'-ccggaattcCCTGAGCCAATTGGTATGGC-3'	EcoRI
SEQ ID NO: 16	R9_449R	5'-cgcggaattcctcAAGGTTCAATGTAACCGCC-3'	BamHI
SEQ ID NO: 17	R9_490F	5'-ccggaattcAAGGATAACTTCACAAATCAG-3'	EcoRI
SEQ ID NO: 18	R9_490R	5'-cgcggaattcctcCTTATCAACACTTTTCATAATA-3'	BamHI
SEQ ID NO: 19	R9_530F	5'-ccggaattcAGAGAAACACTAATTAGCTTA-3'	EcoRI
SEQ ID NO: 20	R9_530R	5'-cgcggaattcctcTCTCAACTCATTGGAATTAAC-3'	BamHI
SEQ ID NO: 21	R9_561F	5'-ccggaattcGGACAAGAAACAATTGAGTC-3'	EcoRI
SEQ ID NO: 7	R9_561R	5'-cgcggaattcctcTCCCTTTTCATTAATAACATTG-3'	BamHI

B.

Cloning of SEQ ID NO: 2 amino acid fragments	Sense primer	Antisense primer
1-599	R9_5E3	R9_3BG
35-599	R9_5E	R9_3BG
35-342	R9_5E	R9_342R
229-402	R9_5E1	R9_402R
229-599	R9_5E1	R9_3BG
380-599	R9_5E2	R9_3BG
380-449	R9_5E2	R9_449R
380-490	R9_5E2	R9_490R
380-530	R9_5E2	R9_530R
380-561	R9_5E2	R9_561R
449-599	R9_449F	R9_3BG
490-599	R9_490F	R9_3BG
530-599	R9_530F	R9_3BG
561-599	R9_561F	R9_3BG